Camille Scott

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By Request
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(as of May 2022)

Education

Alma College, Alma, MI — 2008-2012
B.S., Computer Science

Michigan State University, East Lansing, MI — 2012-2015
GED Lab, PhD. student, Computer Science

University of California Davis, Davis, CA — 2015-2022
PhD., Computer Science, Lab for Data Intensive Biology
Dissertation: Streaming Methods for Assembly Graph Analysis

Honors and Awards

National Merit Finalist	2008
Alma College / Distinguished Scholar Award	2008-2012
Binghamton University / Research Experience for Undergrads	2011
USDA / MSU / National Needs Fellow	2013-2015

Manuscripts

Scott, C., & Brown, C. T. (2022). *Streaming Construction of the Compact de Bruijn Graph.* In prep.

Reiter, T., Brooks, P. T., Irber, L., Joslin, S. E., Reid, C. M., Scott, C., ... & Pierce, N. T. (2020). *Streamlining Data-Intensive Biology With Workflow Systems.*. BioRxiv.

Neches, R. Y., & Scott, C. (2018). *SuchTree: Fast, thread-safe computations with phylogenetic trees.* Journal of Open Source Software, 3(26), 678.

Scott, C. (2017). *shmlast: An improved implementation of Conditional Reciprocal Best Hits with LAST and Python.* The Journal of Open Source Software, 2017.

Ren, J., Chung-Davidson, Y. W., Yeh, C. Y., Scott, C., Brown, T., & Li, W. (2015). *Genome-wide analysis of the ATP-binding cassette (ABC) transporter gene family in sea lamprey and Japanese lamprey.* BMC genomics, 16(1), 436.

Crusoe, M. R. et. al. (2015). *The khmer software package: enabling efficient nucleotide sequence analysis.* F1000Research, 4.

Aleksic, J., Alexa, A., Attwood, T. K., Hong, N. C., Dahlö, M., Davey, R., ..., & Lahti, L. (2014) *The open science peer review oath.* F1000Research, 3.

Blogs and social media

Blog: camillescott.org

Twitter: @camille_codon

GitHub: github.com/camillescott

Professional Activities

Teaching Assistant (TA) at **Alma College**,
Intro to Computer Science 2011-2012

Co-founder, **Alma College Association for Computing Machinery** 2012

Lead Instructor/TA at **Michigan State University**,
CSE 101 Fall 2012

Presenter at **Michigan State University**,
Summer Research Opportunities (SROP) Workshop 5/2013

TA for workshop at **Marine Biological Laboratory**,
Strategies and Techniques for Analyzing Microbial Population Structures 8/2013

TA for workshop at **California Institute of Technology**,
Workshop on Microbial Bioinformatics 10/2013

TA for SROP Workshop at **Michigan State University**,
Statistics Bootcamp 05/2014

Participant in Workshop at **The Genome Analysis Center (TGAC)**,
AllBio Open Science & Reproducibility Best Practices Workshop 09/2014

Participant in Workshop at **University of California Davis**,
Software Carpentry "Train the Trainers" 01/2015

Lead Instructor for workshop at **UC Davis**,
ANGUS: Next-Gen Sequence Analysis Workshop Summer 2017

TA at **UC Davis**,
ECS132: Probabilistic and Statistical Modeling in Computer Science Spring 2021

Software

Contributor to **khmer Protocols Project**,
Protocols for cloud-based de novo RNA-seq and metagenomic analyses
khmer-protocols.readthedocs.org

Contributor to open source **khmer software package**,
k-mer counting, graph traversal, and sequence processing
github.com/dib-lab/khmer

Member of and contributor to **bioconda channel**,
conda channel for bioinformatics packages for Linux and MacOS
github.com/bioconda/bioconda-recipes

Author and maintainer of **goetia**,
C++ and Python library and command line tools for streaming sequence analysis
github.com/camillescott/goetia

Author and maintainer of **debruijnal-enhance-o-tron**,
pytest fixtures for random de Bruijn graph generation
github.com/camillescott/debruijnal-enhance-o-tron

Author and maintainer of **dammit**,
a tool for easy de novo transcriptome annotation
github.com/camillescott/dammit

Author and maintainer of **shmlast**,
an implementation of conditional reciprocal best hits with Python and LAST
github.com/camillescott/shmnlast

References

(Contact details available upon request)